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<110> Cohen, Bruce D.
      Beebe, Jean
      Miller, Penelope E.
      Moyer, James D.
      Corvalan, Jose R.
      Gallo, Michael
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
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accateteca gggacaacge caagaactea etgtatetge aaatgaacag cetgagagee 240
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Thr Arg Asp Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Gly Val Glu Thr Thr
Phe Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
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aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
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Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
Tyr Ala Ala Ser Arg Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly
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Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala Asp Ser Val Lys
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr Leu
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tatgctgcat cccgtttaca aagtggggtc ccatcaaggt tcagcggcag tggatctggg 180
acagaattca ctctcacaat cagcagectg cageetgaag attttgcaae ttattactgt 240
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Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser
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Gly Val Pro Ser Arg	g Phe Ser Gly Ser G. 55	ly Ser Gly Thr Gl 60	u Phe Thr
Leu Thr Ile Ser Ser 65	Leu Gln Pro Glu A: 70	sp Phe Ala Thr Ty 75	r Tyr Cys 80
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Glu Ile Ile Arg 100			
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Ser Pro Asn Tyr Asn 50	Pro Ser Leu Lys Se 55	er Arg Val Thr Me	t Ser Val
Asp Thr Ser Lys Asn 65	Gln Phe Ser Leu Ly	ys Leu Asn Ser Va 75	l Thr Ala 80
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Tyr Ala Ala Ser Lys Leu His Arg Gly Val Pro Ser Arg Phe Ser Gly
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Arg Leu Gln Pro
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Ile His Val Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
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Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser 35 40 45

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp 50 55

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala 65 70 75 80

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
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Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
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Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
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Pro 225	Gln	Val	Tyr	Thr	Leu 230	Pro	Pro	Ser	Arg	Glu 235	Glu	Met	Thr	Lys	Asn 240	
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Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
                                      10
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
Lys Ser Arg Val Thr Ile Ser Val Asp Lys Ser Lys Asn Gln Phe Ser
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                                      90
Ala Arg
<210> 35
<211> 293
<212> DNA
<213> Homo sapiens
<400> 35
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagetgaget etgtgaeege tgeggaeaeg geegtgtatt aetgtgegag aga
<210> 36
<211> 97
<212> PRT
<213> Homo sapiens
<400> 36
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
             20
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
                             40
```

```
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 Arg
 <210> 37
 <211> 290
 <212> DNA
 <213> Homo sapiens
<400> 37
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctcc
<210> 38
<211> 96
<212> PRT
<213> Homo sapiens
<400> 38
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
<210> 39
<211> 288
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (288)
<223> a, c, t, g, other or unknown
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<400> 39
 gacatecaga tgacecagte tecatectee etgtetgeat etgtaggaga eagagteace 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctacag cataatagtt accctccn
                                                                    288
 <210> 40
 <211> 96
 <212> PRT
 <213> Homo sapiens
 <400> 40
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
<210> 41
<211> 288
<212> DNA
<213> Homo sapiens
<400> 41
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaageee etaageteet gatetatget geateeagtt tgeaaagtgg ggteeeatea 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcch
                                                                   288
<210> 42
<211> 96
<212> PRT
<213> Homo sapiens
<400> 42
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
```

J J			4 0

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

Glu Asp Phe Ala Thr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro 85 90 95

<210> 43

<211> 293

<212> DNA

<213> Homo sapiens

<400> 43

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60 acctgcactg tctctggtgg ctccatcagt agttactact ggagctggat ccggcagccc 120 gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcac caactacaac 180 ccctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240 aagctgagct ctgtgaccgc cgcggacacg gccgtgtatt actgtgcgag aga 293

<210> 44

<211> 97

<212> PRT

<213> Homo sapiens

<400> 44

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile 35 40 45

Gly Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala 85 90

Arg

<210> 45

<211> 470

<212> PRT

<213> Homo sapiens

<400> 45

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Thr Thr Phe Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Leu Gly Trp Ser Asp Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr 170 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 200 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys 230 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp 280 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp 330 325

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 370 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415 \hspace{1.5cm}$

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 450 460

Ser Leu Ser Pro Gly Lys 465 470

<210> 46

<211> 470

<212> PRT

<213> Homo sapiens

<400> 46

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly 1 5 10 15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 100 105 110

Tyr Tyr Cys Ala Lys Gly Tyr Ser Ser Gly Trp Tyr Tyr Tyr Tyr Tyr 115 120 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

	130					135					140				
Ala 145	Ser	Thr	Lys	Gly	Pro 150	Ser	Val	Phe	Pro	Leu 155	Ala	Pro	Cys	Ser	Arg 160
Ser	Thr	Ser	Glu	Ser 165	Thr	Ala	Ala	Leu	Gly 170	Cys	Leu	Val	Lys	Asp 175	Tyr
Phe	Pro	Glu	Pro 180	Val	Thr	Val	Ser	Trp 185	Asn	Ser	Gly	Ala	Leu 190	Thr	Ser
Gly	Val	His 195	Thr	Phe	Pro	Ala	Val 200	Leu	Gln	Ser	Ser	Gly 205	Leu	Tyr	Ser
Leu	Ser 210	Ser	Val	Val	Thr	Val 215	Pro	Ser	Ser	Asn	Phe 220	Gly	Thr	Gln	Thr
Tyr 225	Thr	Cys	Asn	Val	Asp 230	His	Lys	Pro	Ser	Asn 235	Thr	Lys	Val	Asp	Lys 240
Thr	Val	Glu	Arg	Lys 245	Cys	Cys	Val	Glu	Cys 250	Pro	Pro	Cys	Pro	Ala 255	Pro
Pro	Val	Ala	Gly 260	Pro	Ser	Val	Phe	Leu 265	Phe	Pro	Pro	Lys	Pro 270	Lys	Asp
Thr	Leu	Met 275	Ile	Ser	Arg	Thr	Pro 280	Glu	Val	Thr	Cys	Val 285	Val	Val	Asp
Val	Ser 290	His	Glu	Asp	Pro	Glu 295	Val	Gln	Phe	Asn	Trp 300	Tyr	Val	Asp	Gly
Val 305	Glu	Val	His	Asn	Ala 310	Lys	Thr	Lys	Pro	Arg 315	Glu	Glu	Gln	Phe	Asn 320
Ser	Thr	Phe	Arg	Val 325	Val	Ser	Val	Leu	Thr 330	Val	Val	His	Gln	Asp 335	Trp
Leu	Asn	Gly	Lys 340	Glu	Tyr	Lys	Cys	Lys 345	Val	Ser	Asn	Lys	Gly 350	Leu	Pro
Ala	Pro	Ile 355	Glu	Lys	Thr	Ile	Ser 360	Lys	Thr	Lys	Gly	Gln 365	Pro	Arg	Glu
Pro	Gln 370		Tyr	Thr	Leu	Pro 375		Ser	Arg		Glu 380	Met	Thr	Lys	Asn
Gln 385	Val	Ser	Leu	Thr	Cys 390	Leu	Val	Lys	Gly	Phe 395	Tyr	Pro	Ser	Asp	Ile 400
Ala	Val	Glu	Trp	Glu 405	Ser	Asn	Gly	Gln	Pro 410	Glu	Asn	Asn	Tyr	Lys 415	Thr
Thr	Pro	Pro	Met 420	Leu	Asp	Ser	Asp	Gly 425	Ser	Phe	Phe	Leu	Tyr 430	Ser	Lys
Leu	Thr	Val 435	Asp	Lys	Ser	Arg	Trp 440	Gln	Gln	Gly	Asn	Val 445	Phe	Ser	Cys
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu

450 455 460

Ser Leu Ser Pro Gly Lys 465 470

<210> 47

<211> 236

<212> PRT

<213> Homo sapiens

<400> 47

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser 35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys 50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu His Arg Gly Val 65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr $85 \\ 90 \\ 95$

Ile Ser Ser Leu Gl
n Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gl
n $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

His Asn Ser Tyr Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu 165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235

<210> 48 <211> 236

<212> PRT <213> Homo sapiens

<400> 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp

1 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser 35 40 45

Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val 65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr 85 90 95

Ile Ser Ser Leu Gl
n Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gl
n 100 105 110

His Asn Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235

<210> 49

<211> 470

<212> PRT

<213> Homo sapiens

<400> 49

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
1 5 10 15

Val Gln Cys Gln Ala Gln Leu Val Glu Ser Gly Gly Leu Val Lys

20 25 30

Pro	Gly	Gly 35	Ser	Leu	Arg	Leu	Ser 40	Cys	Ala	Ala	Ser	Gly 45	Phe	Thr	Phe
Ser	Asp 50	Tyr	Tyr	Met	Ser	Trp 55	Ile	Arg	Gln	Ala	Pro 60	Gly	Lys	Gly	Leu
Glu 65	Trp	Val	Ser	Tyr	Ile 70	Ser	Ser	Ser	Gly	Ser 75	Thr	Arg	Asp	Tyr	Ala 80
Asp	Ser	Val	Lys	Gly 85	Arg	Phe	Thr	Ile	Ser 90	Arg	Asp	Asn	Ala	Lys 95	Asn
Ser	Leu	Tyr	Leu 100	Gln	Met	Asn	Ser	Leu 105	Arg	Ala	Glu	Asp	Thr 110	Ala	Val
Tyr	Tyr	Cys 115	Val	Arg	Asp	Gly	Val 120	Glu	Thr	Thr	Phe	Tyr 125	Tyr	Tyr	Tyr
Tyr	Gly 130	Met	Asp	Val	Trp	Gly 135	Gln	Gly	Thr	Thr	Val 140	Thr	Val	Ser	Ser
Ala 145	Ser	Thr	Lys	Gly	Pro 150	Ser	Val	Phe	Pro	Leu 155	Ala	Pro	Cys	Ser	Arg 160
Ser	Thr	Ser	Glu	Ser 165	Thr	Ala	Ala	Leu	Gly 170	Cys	Leu	Val	Lys	Asp 175	Tyr
Phe	Pro	Glu	Pro 180	Val	Thr	Val	Ser	Trp 185	Asn	Ser	Gly	Ala	Leu 190	Thr	Ser
Gly	Val	His 195	Thr	Phe	Pro	Ala	Val 200	Leu	Gln	Ser	Ser	Gly 205	Leu	Tyr	Ser
Leu	Ser 210	Ser	Val	Val	Thr	Val 215	Pro	Ser	Ser	Asn	Phe 220	Gly	Thr	Gln	Thr
Tyr 225	Thr	Cys	Asn	Val	Asp 230	His	Lys	Pro	Ser	Asn 235	Thr	Lys	Val	Asp	Lys 240
Thr	Val	Glu	Arg	Lys 245	Cys	Cys	Val	Glu	Cys 250	Pro	Pro	Cys	Pro	Ala 255	Pro
Pro	Val	Ala	Gly 260	Pro	Ser	Val	Phe	Leu 265	Phe	Pro	Pro	Lys	Pro 270	Lys	Asp
Thr	Leu	Met 275	Ile	Ser	Arg	Thr	Pro 280	Glu	Val	Thr	Cys	Val 285	Val	Val	Asp
Val	Ser 290	His	Glu	Asp	Pro	Glu 295	Val	Gln	Phe	Asn	Trp 300	Tyr	Val	Asp	Gly
Val 305	Glu	Val	His	Asn	Ala 310	Lys	Thr	Lys	Pro	Arg 315	Glu	Glu	Gln	Phe	Asn 320
Ser	Thr	Phe	Arg	Val 325	Val	Ser	Val	Leu	Thr 330	Val	Val	His	Gln	Asp 335	Trp
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro

340	345	350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 450 460

Ser Leu Ser Pro Gly Lys 465 470

<210> 50

<211> 473

<212> PRT

<213> Homo sapiens

<400> 50

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
1 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30 \hspace{1.5cm}$

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 35 40 45

Ser Asp Tyr Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu 50 60

Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Thr Ile Tyr Tyr Ala 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Tyr Tyr Cys Ala Arg Val Leu Arg Phe Leu Glu Trp Leu Leu Tyr Tyr 115 120 125

Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr 130 135 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly 200 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly 215 Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 265 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 295 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met 375 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu 425 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 455

```
Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470
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<210> 51

<211> 236

<212> PRT

<213> Homo sapiens

<400> 51

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Phe Thr Cys Arg Ala Ser 35 40 45

Gln Asp Ile Arg Arg Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val 65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr 85 90 95

Ile Ser Ser Leu Gl
n Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gl
n 100 105 110

His Asn Asn Tyr Pro Arg Thr Phe Gly Gln Gly Thr Glu Val Glu Ile 115 120 125

Ile Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235

<210> 52

<211> 236

<212> PRT

<213> Homo sapiens

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<400> 52
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
                                105
His Asn Ser Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                        135
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180
                                185
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                        215
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                    230
<210> 53
<211> 326
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Consensus
     sequence
<220>
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<221> modified base

<222> (289)

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<223> a, c, t, g, other or unknown
gacatccaga tgacccagty tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
wtcacttgcc gggcaagtca ggrcattaga mrtgatttag gctggtwtca gcagaaacca 120
gggaaageye ctaagegeet gatetatget geateemrwt treammgwgg ggteecatea 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcmg cctgcagcct 240
gaagattttg caacttatta ctgtytacar cataatartt aycckybsns kttyggcsrr 300
gggaccrags tggaratcaw acgaac
                                                                   326
<210> 54
<211> 322
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Consensus
      sequence
<400> 54
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgyaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagy asctwtttaa attggtatca gcagaaacca 120
gggaaagccc ctaarctcct gatcyatgyt gcatccagtt trcaargtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacartr ccccayychc tttcggcgga 300
gggaccaagg tggagatcaa ac
                                                                   322
<210> 55
<211> 325
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Consensus
      sequence
<220>
<221> modified base
<222> (291)
<223> a, c, t, g, other or unknown
<400> 55
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgya gggccagtca gagtgttmgc rgcagstact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat qqtqcatcca qcaqqqccac tqqcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtw ttactgtcag cagtatggta gytcacctcs nacgttcggc 300
caagggacca aggtggaaat caaac
                                                                   325
<210> 56
<211> 376
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Consensus
      sequence
```

```
<400> 56
caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60
teetgtgeag eetetggatt eacytteagt gactactaya tgagetggat eegecagget 120
ccagggaagg ggctggartg ggtttcatac attagtagta gtggtagtac cakakactac 180
gcagactetg tgaagggeec atteaceate tecagggaea acgeeaagaa eteaetgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgy gagagatgga 300
gtggaaacta ctttttacta ctactactac ggtatggacg tctggggcca agggaccacg 360
gtcaccgtct cctcag
<210> 57
<211> 358
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Consensus
      sequence
<220>
<221> modified_base
<222> (337)
<223> a, c, t, g, other or unknown
<400> 57
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tetetggtgg etecateagt arttactact ggagetggat eeggeageee 120
gccgggaagg gactggagtg gattgggcgt atctatacca gtgggagcmc caactacaac 180
ccctccctca agagtcgagt caccatgtca gtagacacgt ccaagaacca gttctccctg 240
aagctgarct ctgtgaccgc cgcggacacg gccgtgtatt actgtgcggt aacgattttt 300
ggagtggtta ttatctttga ctactggggc cagrganccc tggtcaccgt ctcctcag
<210> 58
<211> 418
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Consensus
      sequence
<400> 58
caggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
teetgtreag cetetggatt cacetttage agetatgeea tgaretgggt eegeeagget 120
ccagggaagg ggctggagtg ggtctcagst attastggka gtggtggtab yacatwctac 180
gcagactccg tgaagggccc gttcaccatc tccagagaca attccargam cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc qaaaqatctk 300
ggctrsksyg actyttacta ctactactac ggtatggacg tctggggcca agggacyacg 360
gtgattatga gttggttcga cccctggggc cagggaaccc tggtcaccgt ctcctcag
<210> 59
<211> 364
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Consensus
```

sequence

```
<400> 59
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttactact ggagytggat ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgact caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagyt ctgtgaccgc tgcggacacg gccgtgtatt actgtgccag gacgtatagc 300
agttegttet actactaegg tatggaegte tggggeeaag ggaecaeggt caeegtetee 360
tcag
                                                                  364
<210> 60
<211> 15
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Gly-Ser Linker
<400> 60
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
```